



## SEQUENCE LISTING

<110> BATEMAN, JOHN  
FITZGERALD, DAVID

<120> A MOLECULAR MARKER

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<141> 2003-10-31

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<151> 2002-05-02

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<170> PatentIn Ver. 3.3

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actctaagca	agaggcctgt	acttttggg	gtttcactgc	acactggcc	tggatctag	4260
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cacac	cattcctcac	agacc	ctgc	gcca	agagtc	4380
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tggactcaca	caaca	taac	cagc	cc	ccctcg	4680
gcttcc	tcctccgg	acctt	gggg	tgg	cc	4740
cccacca	cagg	gcgt	at	cc	cc	4800
gtgcgg	ggc	ttt	cc	cc	cc	4860
ggaaactga	ggc	ttt	cc	cc	cc	4920
gatccc	ggc	ttt	cc	cc	cc	4980
cctgg	ggc	ttt	cc	cc	cc	5040
ggctcc	gc	ttt	cc	cc	cc	5100
gcccgg	gc	ttt	cc	cc	cc	5160
ctcac	tc	ttt	cc	cc	cc	5220
cggcgt	gg	ttt	cc	cc	cc	5280

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<210> 20  
<211> 418  
<212> PRT  
<213> Homo sapiens

<400> 20			
Met Leu Pro Trp Thr Ala Leu Gly Leu Ala Leu Ser Leu Arg Leu Ala			
1	5	10	15
Leu Ala Arg Ser Gly Ala Glu Arg Gly Pro Pro Ala Ser Ala Pro Arg			
20	25	30	
Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr			
35	40	45	
Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu			
50	55	60	
Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser			
65	70	75	80
Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala			
85	90	95	
Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His			
100	105	110	
Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala			
115	120	125	
Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp			
130	135	140	
Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp			
145	150	155	160
Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu			
165	170	175	
Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe			
180	185	190	
Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser			
195	200	205	
Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr			
210	215	220	
Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser			
225	230	235	240

Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro Gly Ala Ala  
 245 250 255  
 Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile Trp Ala Gly  
 260 265 270  
 Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro Glu Ser Asn  
 275 280 285  
 Val Arg Leu Leu Arg Pro Gln Ile Leu Arg Val Arg Thr Arg Pro Glu  
 290 295 300  
 Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser  
 305 310 315 320  
 Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Ser Ala Ala Ala Leu Gly  
 325 330 335  
 Tyr His Val Gln Phe Gly Pro Leu Arg Gly Gly Glu Ala Gln Arg Val  
 340 345 350  
 Glu Val Pro Ala Gly Arg Asn Cys Thr Thr Leu Gln Gly Leu Ala Pro  
 355 360 365  
 Gly Thr Ala Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg  
 370 375 380  
 Glu Ser Ala Leu Ser Ala Lys Ala Cys Thr Pro Asp Gly Pro Arg Pro  
 385 390 395 400  
 Arg Pro Arg Pro Val Pro Arg Ala Pro Thr Pro Gly Thr Ala Ser Arg  
 405 410 415  
 Glu Pro

<210> 21  
<211> 415  
<212> PRT  
<213> *Mus musculus*

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<400> 21
Met Leu Phe Trp Thr Ala Phe Ser Met Ala Leu Ser Leu Arg Leu Ala
      1           5           10          15

Leu Ala Arg Ser Ser Ile Glu Arg Gly Ser Thr Ala Ser Asp Pro Gln
      20          25          30

Gly Asp Leu Leu Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr
      35          40          45

Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Thr Met
      50          55          60

Ser Phe Gly Pro Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
      65          70          75          80

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Gln Pro His Thr Glu Phe Thr Phe Asp Gln Tyr Ser Ser Gly Gln Ala  
                   85                         90                         95  
 Ile Arg Asp Ala Ile Arg Val Ala Pro Gln Arg Met Gly Asp Thr Asn  
                   100                     105                         110  
 Thr Gly Leu Ala Leu Ala Tyr Ala Lys Glu Gln Leu Phe Ala Glu Glu  
                   115                     120                         125  
 Ala Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp  
                   130                     135                         140  
 Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp  
                   145                     150                     155                 160  
 Leu Gly Val Thr Ile Phe Ile Val Ser Thr Gly Arg Gly Asn Leu Leu  
                   165                     170                         175  
 Glu Leu Leu Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe  
                   180                     185                         190  
 Val Asp Val Asp Asp Leu Pro Ile Ile Ala Arg Glu Leu Arg Gly Ser  
                   195                     200                         205  
 Ile Thr Asp Ala Met Gln Pro Gln Gln Leu His Ala Ser Glu Val Leu  
                   210                     215                         220  
 Ser Ser Gly Phe Arg Leu Ser Trp Pro Pro Leu Leu Thr Ala Asp Ser  
                   225                     230                     235                 240  
 Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Gly Lys Leu Ala Thr Thr  
                   245                     250                         255  
 Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Ser Trp Thr Trp Thr Asp  
                   260                     265                         270  
 Leu Asp Pro Asp Thr Asp Tyr Glu Val Ser Leu Leu Pro Glu Ser Asn  
                   275                     280                         285  
 Val His Leu Leu Arg Pro Gln His Val Arg Val Arg Thr Leu Gln Glu  
                   290                     295                         300  
 Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser  
                   305                     310                     315                 320  
 Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Pro Asp Ser Ala Leu Gly  
                   325                     330                         335  
 Tyr His Val Gln Leu Gly Pro Leu Gln Gly Gly Ser Leu Glu Arg Val  
                   340                     345                         350  
 Glu Val Pro Ala Gly Gln Asn Ser Thr Thr Val Gln Gly Leu Thr Pro  
                   355                     360                         365  
 Cys Thr Thr Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg  
                   370                     375                         380

Gln Arg Ala Leu Ser Ala Lys Ala Cys Thr Ala Ser Gly Ala Arg Thr  
 385                   390                   395                   400

Arg Ala Pro Gln Ser Met Arg Pro Glu Ala Gly Pro Arg Glu Pro  
 405                   410                   415

<210> 22  
 <211> 182  
 <212> PRT  
 <213> Gullus gallus

<400> 22  
 Ile Ala Asp Ile Val Ile Leu Val Asp Gly Ser Trp Ser Ile Gly Arg  
 1               5               10               15

Phe Asn Phe Arg Leu Val Arg Leu Phe Leu Glu Asn Leu Val Ser Ala  
 20               25               30

Phe Asn Val Gly Ser Glu Lys Thr Arg Val Gly Leu Ala Gln Tyr Ser  
 35               40               45

Gly Asp Pro Arg Ile Glu Trp His Leu Asn Ala Tyr Gly Thr Lys Asp  
 50               55               60

Ala Val Leu Asp Ala Val Arg Asn Leu Pro Tyr Lys Gly Gly Asn Thr  
 65               70               75               80

Leu Thr Gly Leu Ala Leu Thr Tyr Ile Leu Glu Asn Ser Phe Lys Pro  
 85               90               95

Glu Ala Gly Ala Arg Pro Gly Val Ser Lys Ile Gly Ile Leu Ile Thr  
 100              105              110

Asp Gly Lys Ser Gln Asp Asp Val Ile Pro Pro Ala Lys Asn Leu Arg  
 115              120              125

Asp Ala Gly Ile Glu Leu Phe Ala Ile Gly Val Lys Asn Ala Asp Ile  
 130              135              140

Asn Glu Leu Lys Glu Ile Ala Ser Glu Pro Asp Ser Thr His Val Tyr  
 145              150              155              160

Asn Val Ala Asp Phe Asn Phe Met Asn Ser Ile Val Glu Gly Leu Thr  
 165              170              175

Arg Thr Val Cys Ser Arg  
 180

<210> 23  
 <211> 183  
 <212> PRT  
 <213> Unknown Sequence

<220>  
 <223> Description of Unknown Sequence: VA domain from  
 Unknown collagen VII

<400> 23  
 Ala Ala Asp Ile Val Phe Leu Leu Asp Gly Ser Ser Ser Ile Gly Arg  
 1 5 10 15

Ser Asn Phe Arg Glu Val Arg Ser Phe Leu Glu Gly Leu Val Leu Pro  
 20 25 30

Phe Ser Gly Ala Ala Ser Ala Gln Gly Val Arg Phe Ala Thr Val Gln  
 35 40 45

Tyr Ser Asp Asp Pro Arg Thr Glu Phe Gly Leu Asp Ala Leu Gly Ser  
 50 55 60

Gly Gly Asp Val Ile Arg Ala Ile Arg Glu Leu Ser Tyr Lys Gly Gly  
 65 70 75 80

Asn Thr Arg Thr Gly Ala Ala Ile Leu His Val Ala Asp His Val Phe  
 85 90 95

Leu Pro Gln Leu Ala Arg Pro Gly Val Pro Lys Val Cys Ile Leu Ile  
 100 105 110

Thr Asp Gly Lys Ser Gln Asp Leu Val Asp Thr Ala Ala Gln Arg Leu  
 115 120 125

Lys Gly Gln Gly Val Lys Leu Phe Ala Val Gly Ile Lys Asn Ala Asp  
 130 135 140

Pro Glu Glu Leu Lys Arg Val Ala Ser Gln Pro Thr Ser Asp Phe Phe  
 145 150 155 160

Phe Phe Val Asn Asp Phe Ser Ile Leu Arg Thr Leu Leu Pro Leu Val  
 165 170 175

Ser Arg Arg Val Cys Thr Thr  
 180

<210> 24  
 <211> 182  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Lys Ala Asp Ile Val Phe Leu Thr Asp Ala Ser Trp Ser Ile Gly Asp  
 1 5 10 15

Asp Asn Phe Asn Lys Val Val Lys Phe Ile Phe Asn Thr Val Gly Ala  
 20 25 30

Phe Asp Glu Val Asn Pro Ala Gly Ile Gln Val Ser Phe Val Gln Tyr  
 35 40 45

Ser Asp Glu Val Lys Ser Glu Phe Lys Leu Asn Thr Tyr Asn Asp Lys  
 50 55 60

Ala Leu Ala Leu Gly Ala Leu Gln Asn Ile Arg Tyr Arg Gly Gly Asn  
 65 70 75 80

Thr Arg Thr Gly Lys Ala Leu Thr Phe Ile Lys Glu Lys Val Leu Thr  
 85 90 95

Trp Glu Ser Gly Met Arg Lys Asn Val Arg Val Leu Gly Val Val Thr  
 100 105 110

Asp Gly Arg Ser Gln Asp Glu Val Lys Lys Ala Ala Phe Val Ile Gln  
 115 120 125

Gln Ser Gly Phe Ser Val Phe Val Val Gly Val Ala Asp Val Asp Tyr  
 130 135 140

Asn Glu Leu Ala Asn Ile Ala Ser Lys Pro Ser Glu Arg His Val Phe  
 145 150 155 160

Ile Val Asp Asp Phe Glu Ser Phe Glu Lys Ile Glu Asp Asn Leu Ile  
 165 170 175

Thr Phe Val Cys Glu Thr  
 180

<210> 25  
 <211> 185  
 <212> PRT  
 <213> Unknown Sequence

<220>  
 <223> Description of Unknown Sequence: VA domain from  
 Unknown collagen VI

<400> 25  
 Ala Ala Asp Ile Val Phe Leu Val Asp Ser Ser Trp Ser Ala Gly Lys  
 1 5 10 15

Asp Arg Phe Leu Leu Val Gln Glu Phe Leu Ser Asp Val Val Glu Ser  
 20 25 30

Leu Ala Val Gly Asp Asn Asp Phe His Phe Ala Leu Val Arg Leu Asn  
 35 40 45

Gly Asn Pro His Thr Glu Phe Leu Leu Asn Thr Tyr His Ser Lys Gln  
 50 55 60

Glu Val Leu Ser His Ile Ala Asn Met Ser Tyr Ile Gly Gly Ser Asn  
 65 70 75 80

Gln Thr Gly Lys Gly Leu Glu Tyr Val Ile His Ser His Leu Thr Glu  
 85 90 95

Ala Ser Gly Ser Arg Ala Ala Asp Gly Val Pro Gln Val Ile Val Val  
 100 105 110

Leu Thr Asp Gly Gln Ser Glu Asp Gly Phe Ala Leu Pro Ser Ala Glu  
 115 120 125

Leu Lys Ser Ala Asp Val Asn Val Phe Ala Val Gly Val Glu Gly Ala  
 130 135 140

Asp Glu Arg Ala Leu Gly Glu Val Ala Ser Glu Pro Leu Leu Ser Met  
 145 150 155 160

His Val Phe Asn Leu Glu Asn Val Thr Ser Leu His Gly Leu Val Gly  
 165 170 175

Asn Leu Val Ser Cys Ile His Ser Ser  
 180 185

<210> 26

<211> 185

<212> PRT

<213> Mus musculus

<400> 26

Arg Ala Asp Leu Val Phe Ile Ile Asp Ser Ser Arg Ser Val Asn Thr  
 1 5 10 15

Tyr Asp Tyr Ala Lys Val Lys Glu Phe Ile Leu Asp Ile Leu Gln Phe  
 20 25 30

Leu Asp Ile Gly Pro Asp Val Thr Arg Val Gly Leu Leu Gln Tyr Gly  
 35 40 45

Ser Thr Val Lys Asn Glu Phe Ser Leu Lys Thr Phe Lys Arg Lys Ser  
 50 55 60

Glu Val Glu Arg Ala Val Lys Arg Met Arg His Leu Ser Thr Gly Thr  
 65 70 75 80

Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu Asn Ile Ala Phe Ser Glu  
 85 90 95

Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn Val Pro Arg Ile Ile Met  
 100 105 110

Ile Val Thr Asp Gly Arg Pro Gln Asp Ser Val Ala Glu Val Ala Ala  
 115 120 125

Lys Ala Arg Asn Thr Gly Ile Leu Ile Phe Ala Ile Gly Val Gly Gln  
 130 135 140

Val Asp Leu Asn Thr Leu Lys Ala Ile Gly Ser Glu Pro His Lys Asp  
 145 150 155 160

His Val Phe Leu Val Ala Asn Phe Ser Gln Ile Glu Ser Leu Thr Ser  
 165 170 175

Val Phe Gln Asn Lys Leu Cys Thr Val  
 180 185

&lt;210&gt; 27

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 27

Pro	Leu	Asp	Leu	Val	Phe	Met	Ile	Asp	Ser	Ser	Arg	Ser	Val	Arg	Pro
1				5					10					15	

Phe	Glu	Phe	Glu	Thr	Met	Arg	Gln	Phe	Leu	Val	Gly	Leu	Leu	Arg	Ser
				20					25				30		

Leu	Asp	Val	Gly	Leu	Asn	Ala	Thr	Arg	Val	Gly	Val	Ile	Gln	Tyr	Ser
				35			40					45			

Ser	Gln	Val	Gln	Ser	Val	Phe	Pro	Leu	Gly	Ala	Phe	Ser	Arg	Arg	Glu
				50			55				60				

Asp	Met	Glu	Arg	Ala	Ile	Arg	Ala	Val	Val	Pro	Leu	Ala	Gln	Gly	Thr
	65				70				75				80		

Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Met	Asn	Val	Ala	Phe	Ser	Glu
				85					90				95		

Ala	Glu	Gly	Ala	Arg	Pro	Ser	Glu	Glu	Arg	Val	Pro	Arg	Val	Leu	Val
				100			105				110				

Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Arg	Val	Ala	Glu	Val	Ala	Ala
	115				120						125				

Gln	Ala	Arg	Ala	Arg	Gly	Ile	Glu	Ile	Tyr	Ala	Val	Gly	Val	Gln	Arg
	130				135					140					

Ala	Asp	Val	Gly	Ser	Leu	Arg	Thr	Met	Ala	Ser	Pro	Pro	Leu	Asp	Gln
	145				150				155				160		

His	Val	Phe	Leu	Val	Glu	Ser	Phe	Asp	Ile	Gln	Glu	Phe	Gly	Leu	Gln
				165				170				175			

Phe	Gln	Gly	Arg	Leu	Cys	Gly	Lys								
				180											

&lt;210&gt; 28

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 28

Pro	Leu	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser	Ser	Arg	Ser	Val	Arg	Pro
1				5					10				15		

Leu	Glu	Phe	Thr	Lys	Val	Lys	Thr	Phe	Val	Ser	Arg	Ile	Ile	Asp	Thr
				20				25				30			

Leu	Asp	Ile	Gly	Ala	Thr	Asp	Thr	Arg	Val	Ala	Val	Val	Asn	Tyr	Ala
		35				40				45					

Ser Thr Val Lys Ile Glu Phe Gln Leu Asn Thr Tyr Ser Asp Lys Gln  
       50                  55                  60

Ala Leu Lys Gln Ala Val Ala Arg Ile Thr Pro Leu Ser Thr Gly Thr  
       65                  70                  75                  80

Met Ser Gly Leu Ala Ile Gln Thr Ala Met Glu Glu Ala Phe Thr Val  
       85                  90                  95

Glu Ala Gly Ala Arg Gly Pro Met Ser Asn Ile Pro Lys Val Ala Ile  
       100                105                110

Ile Val Thr Asp Gly Arg Pro Gln Asp Gln Val Asn Glu Val Ala Ala  
       115                120                125

Arg Ala Arg Ala Ser Gly Ile Glu Leu Tyr Ala Val Gly Val Asp Arg  
       130                135                140

Ala Asp Met Glu Ser Leu Lys Met Met Ala Ser Lys Pro Leu Glu Glu  
       145                150                155                160

His Val Phe Tyr Val Glu Thr Tyr Gly Val Ile Glu Lys Leu Ser Ala  
       165                170                175

Arg Phe Gln Glu Thr Pro Cys Ala Leu  
       180                185

<210> 29  
 <211> 185  
 <212> PRT  
 <213> Mus musculus

<400> 29  
 Pro Thr Asp Leu Val Phe Val Val Asp Ser Ser Arg Ser Val Arg Pro  
       1                  5                  10                  15

Val Glu Phe Glu Lys Val Lys Val Phe Leu Ser Gln Val Ile Glu Ser  
       20                25                  30

Leu Asp Val Gly Pro Asn Ala Thr Arg Val Gly Leu Val Asn Tyr Ala  
       35                40                  45

Ser Thr Val Lys Pro Glu Phe Pro Leu Arg Ala His Gly Ser Lys Ala  
       50                55                  60

Ser Leu Leu Gln Ala Val Arg Arg Ile Gln Pro Leu Ser Thr Gly Thr  
       65                70                  75                  80

Met Thr Gly Leu Ala Leu Gln Phe Ala Ile Thr Lys Ala Leu Ser Asp  
       85                90                  95

Ala Glu Gly Gly Arg Ala Arg Ser Pro Asp Ile Ser Lys Val Val Ile  
       100               105                110

Val Val Thr Asp Gly Arg Pro Gln Asp Ser Val Arg Asp Val Ser Glu  
       115               120                125

Arg Ala Arg Ala Ser Gly Ile Glu Leu Phe Ala Ile Gly Leu Gly Arg  
 130 135 140  
 Val Asp Lys Ala Thr Leu Arg Gln Ile Ala Ser Glu Pro Gln Asp Glu  
 145 150 155 160  
 His Val Asp Tyr Val Glu Ser Tyr Asn Val Ile Glu Lys Leu Ala Lys  
 165 170 175  
 Lys Phe Gln Glu Ala Phe Cys Val Val  
 180 185

<210> 30  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Gln Leu Asp Ile Val Ile Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro  
 1 5 10 15

Trp Asp Ser Val Thr Ala Phe Leu Asn Asp Leu Leu Lys Arg Met Asp  
 20 25 30

Ile Gly Pro Lys Gln Thr Gln Val Gly Ile Val Gln Tyr Gly Glu Asn  
 35 40 45

Val Thr His Glu Phe Asn Leu Asn Lys Tyr Ser Ser Thr Glu Glu Val  
 50 55 60

Leu Val Ala Ala Lys Lys Ile Val Gln Arg Gly Gly Arg Gln Thr Met  
 65 70 75 80

Thr Ala Leu Gly Thr Asp Thr Ala Arg Lys Glu Ala Phe Thr Glu Ala  
 85 90 95

Arg Gly Ala Arg Arg Gly Val Lys Lys Val Met Val Ile Val Thr Asp  
 100 105 110

Gly Glu Ser His Asp Asn His Arg Leu Lys Lys Val Ile Gln Asp Cys  
 115 120 125

Glu Asp Glu Asn Ile Gln Arg Phe Ser Ile Ala Ile Leu Gly Ser Tyr  
 130 135 140

Asn Arg Gly Asn Leu Ser Thr Glu Lys Phe Val Glu Glu Ile Lys Ser  
 145 150 155 160

Ile Ala Ser Glu Pro Thr Glu Lys His Phe Phe Asn Val Ser Asp Glu  
 165 170 175

Leu Ala Leu Val Thr Ile Val Lys Thr Leu Gly Glu Arg Ile Phe Ala  
 180 185 190

Leu

<210> 31  
<211> 181  
<212> PRT  
<213> Unknown Sequence

<220>  
<223> Description of Unknown Sequence: VA domain from  
Unknown WARP

<400> 31  
Gln Gly Asp Leu Leu Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His  
1 5 10 15  
Tyr Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Thr  
20 25 30  
Met Ser Phe Gly Pro Gly Ala Leu Arg Ala Ser Leu Val His Val Gly  
35 40 45  
Ser Gln Pro His Thr Glu Phe Thr Phe Asp Gln Tyr Ser Ser Gly Gln  
50 55 60  
Ala Ile Arg Asp Ala Ile Arg Val Ala Pro Gln Arg Met Gly Asp Thr  
65 70 75 80  
Asn Thr Gly Leu Ala Leu Ala Tyr Ala Lys Glu Gln Leu Phe Ala Glu  
85 90 95  
Glu Ala Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr  
100 105 110  
Asp Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys  
115 120 125  
Asp Leu Gly Val Thr Ile Phe Ile Val Ser Thr Gly Arg Gly Asn Leu  
130 135 140  
Leu Glu Leu Leu Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His  
145 150 155 160  
Phe Val Asp Val Asp Asp Leu Pro Ile Ile Ala Arg Glu Leu Arg Gly  
165 170 175  
Ser Ile Thr Asp Ala  
180

<210> 32  
<211> 184  
<212> PRT  
<213> Unknown Sequence

<220>  
<223> Description of Unknown Sequence: VA domain from  
Unknown cochlin

<400> 32  
Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Tyr Asn Ile Gly Gln  
1 5 10 15

Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala Val Met  
20 25 30

Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Val Val Gln Ala Ser  
35 40 45

Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ala Ala Lys  
50 55 60

Glu Val Leu Phe Ala Ile Lys Glu Leu Gly Phe Arg Gly Gly Asn Ser  
65 70 75 80

Asn Thr Gly Lys Ala Leu Lys His Ala Ala Gln Lys Phe Phe Ser Met  
85 90 95

Glu Asn Gly Ala Arg Lys Gly Ile Pro Lys Ile Ile Val Val Phe Leu  
100 105 110

Asp Gly Trp Pro Ser Asp Asp Leu Glu Glu Ala Gly Ile Val Ala Arg  
115 120 125

Glu Phe Gly Val Asn Val Phe Ile Val Ser Ser Val Ala Lys Pro Thr  
130 135 140

Thr Glu Glu Leu Gly Met Val Gln Asp Ile Gly Phe Ile Asp Lys Ala  
145 150 155 160

Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr Gln Met Pro Ser Trp Phe  
165 170 175

Gly Thr Thr Lys Tyr Val Lys Pro  
180

<210> 33  
<211> 186  
<212> PRT  
<213> Unknown Sequence

<220>  
<223> Description of Unknown Sequence: VA domain from  
Unknown vwf

<400> 33  
Leu Leu Asp Leu Val Phe Leu Leu Asp Gly Ser Ser Arg Leu Ser Glu  
1 5 10 15

Ala Glu Phe Glu Val Leu Lys Ala Phe Val Val Asp Met Met Glu Arg  
20 25 30

Leu Arg Ile Ser Gln Lys Trp Val Arg Val Ala Val Val Glu Tyr His  
35 40 45

Asp Gly Ser His Ala Tyr Ile Gly Leu Lys Asp Arg Lys Arg Pro Ser  
       50                  55                  60

Glu Leu Arg Arg Ile Ala Ser Gln Val Lys Tyr Ala Gly Ser Gln Val  
       65                  70                  75                  80

Ala Ser Thr Ser Glu Val Leu Lys Tyr Thr Leu Phe Gln Ile Phe Ser  
       85                  90                  95

Lys Ile Asp Arg Pro Glu Ala Ser Arg Ile Ala Leu Leu Leu Met Ala  
       100                 105                 110

Ser Gln Glu Pro Gln Arg Met Ser Arg Asn Phe Val Arg Tyr Val Gln  
       115                 120                 125

Gly Leu Lys Lys Lys Val Ile Val Ile Pro Val Gly Ile Gly Pro  
       130                 135                 140

His Ala Asn Leu Lys Gln Ile Arg Leu Ile Glu Lys Gln Ala Pro Glu  
       145                 150                 155                 160

Asn Lys Ala Phe Val Leu Ser Ser Val Asp Glu Leu Glu Gln Gln Arg  
       165                 170                 175

Asp Glu Ile Val Ser Tyr Leu Cys Asp Leu  
       180                 185

<210> 34  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Pro Arg Asn Leu Lys Val Thr Asp Glu Thr Thr Asp Ser Phe Lys Ile  
       1                  5                  10                 15

Thr Trp Thr Gln Ala Pro Gly Arg Val Leu Arg Tyr Arg Ile Ile Tyr  
       20                 25                 30

Arg Pro Val Ala Gly Gly Glu Ser Arg Glu Val Thr Thr Pro Pro Asn  
       35                 40                 45

Gln Arg Arg Arg Thr Leu Glu Asn Leu Ile Pro Asp Thr Lys Tyr Glu  
       50                 55                 60

Val Ser Val Ile Pro Glu Tyr Phe Ser Gly Pro Gly Thr Pro Leu Thr  
       65                 70                 75                 80

Gly Asn Ala Ala Thr  
       85

<210> 35  
 <211> 86  
 <212> PRT  
 <213> Mus musculus

<400> 35  
 Pro Ser Gln Met Gln Val Thr Asp Val Gln Asp Asn Ser Ile Ser Val  
 1 5 10 15  
 Arg Trp Leu Pro Ser Thr Ser Pro Val Thr Gly Tyr Arg Val Thr Thr  
 20 25 30  
 Thr Pro Lys Asn Gly Leu Gly Pro Ser Lys Thr Lys Thr Ala Ser Pro  
 35 40 45  
 Asp Gln Thr Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr  
 50 55 60  
 Val Val Ser Val Tyr Ala Gln Asn Arg Asn Gly Glu Ser Gln Pro Leu  
 65 70 75 80  
 Val Gln Thr Ala Val Thr  
 85

<210> 36  
 <211> 87  
 <212> PRT  
 <213> Unknown Sequence

<220>  
 <223> Description of Unknown Sequence: F3-2 repeats from  
 Unknown WARP

<400> 36  
 Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser Leu Arg Val  
 1 5 10 15  
 Ser Trp Ala Pro Ala Leu Gly Pro Asp Ser Ala Leu Gly Tyr His Val  
 20 25 30  
 Gln Leu Gly Pro Leu Gln Gly Gly Ser Leu Glu Arg Val Glu Val Pro  
 35 40 45  
 Ala Gly Gln Asn Ser Thr Thr Val Gln Gly Leu Thr Pro Cys Thr Thr  
 50 55 60  
 Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg Gln Arg Ala  
 65 70 75 80  
 Leu Ser Ala Lys Ala Cys Thr  
 85

<210> 37  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 37  
 Pro Thr Arg Leu Val Phe Ser Ala Leu Gly Pro Thr Ser Leu Arg Val  
 1 5 10 15

Ser Trp Gln Glu Pro Arg Cys Glu Arg Pro Leu Gln Gly Tyr Ser Val  
                   20                  25                  30  
 Glu Tyr Gln Leu Leu Asn Gly Gly Glu Leu His Arg Leu Asn Ile Pro  
                   35                  40                  45  
 Asn Pro Ala Gln Thr Ser Val Val Val Glu Asp Leu Leu Pro Asn His  
                   50                  55                  60  
 Ser Tyr Val Phe Arg Val Arg Ala Gln Ser Gln Glu Gly Trp Gly Arg  
                   65                  70                  75                  80  
 Glu Arg Glu Gly Val Ile Thr Ile  
                   85

<210> 38  
 <211> 85  
 <212> PRT  
 <213> Gullus gallus

<400> 38  
 Pro Gln His Leu Glu Val Asp Glu Ala Ser Thr Asp Ser Phe Arg Val  
     1              5                  10                  15  
 Ser Trp Lys Pro Thr Ser Ser Asp Ile Ala Phe Tyr Arg Leu Ala Trp  
     20                  25                  30  
 Ile Pro Leu Asp Gly Gly Glu Ser Glu Glu Val Val Leu Ser Gly Asp  
     35                  40                  45  
 Ala Asp Ser Tyr Val Ile Glu Gly Leu Leu Pro Asn Thr Glu Tyr Glu  
     50                  55                  60  
 Val Ser Leu Leu Ala Val Phe Asp Asp Glu Thr Glu Ser Glu Val Val  
     65                  70                  75                  80  
 Ala Val Leu Gly Ala  
     85

<210> 39  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 39  
 Pro Lys Asp Ile Thr Ile Ser Asn Val Thr Lys Asp Ser Val Met Val  
     1              5                  10                  15  
 Ser Trp Ser Pro Pro Val Ala Ser Phe Asp Tyr Tyr Arg Val Ser Tyr  
     20                  25                  30  
 Arg Pro Thr Gln Val Gly Arg Leu Asp Ser Ser Val Val Pro Asn Thr  
     35                  40                  45  
 Val Thr Glu Phe Thr Ile Thr Arg Leu Asn Pro Ala Thr Glu Tyr Glu  
     50                  55                  60

Ile Ser Leu Asn Ser Val Arg Gly Arg Glu Glu Ser Glu Arg Ile Cys  
 65                    70                    75                    80

Thr Leu Val His Thr  
 85

<210> 40  
 <211> 87  
 <212> PRT  
 <213> Unknown Sequence

<220>  
 <223> Description of Unknown Sequence: F3-1 repeat from  
 Unknown WARP

<400> 40  
 Pro Gln Gln Leu His Ala Ser Glu Val Leu Ser Ser Gly Phe Arg Leu  
 1                5                10                15

Ser Trp Pro Pro Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu  
 20                25                30

Leu Val Pro Ser Gly Lys Leu Ala Thr Thr Arg Arg Gln Gln Leu Pro  
 35                40                45

Gly Asn Ala Thr Ser Trp Thr Trp Thr Asp Leu Asp Pro Asp Thr Asp  
 50                55                60

Tyr Glu Val Ser Leu Leu Pro Glu Ser Asn Val His Leu Leu Arg Pro  
 65                70                75                80

Gln His Val Arg Val Arg Thr  
 85

<210> 41  
 <211> 2311  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (30)..(1274)

<400> 41  
 tcgatcaaga gccccccact ccaggcgcg atg ctg ttc tgg act gcg ttc agc      53  
 Met Leu Phe Trp Thr Ala Phe Ser  
 1                5

atg gct ttg agt ctg cgg ttg gca ttg gcg cgg agc agc ata gag cgc      101  
 Met Ala Leu Ser Leu Arg Leu Ala Leu Ala Arg Ser Ser Ile Glu Arg  
 10                15                20

ggt tcc aca gca tca gac ccc cag ggg gac ctg ttg ttc ctg ttg gac      149  
 Gly Ser Thr Ala Ser Asp Pro Gln Gly Asp Leu Leu Phe Leu Leu Asp  
 25                30                35                40

agc tca gcc agc gtg tca cac tat gag ttc tca aga gtt cgg gaa ttt		197
Ser Ser Ala Ser Val Ser His Tyr Glu Phe Ser Arg Val Arg Glu Phe		
45	50	55
gtg ggg cag ctg gtg gct acg atg tct ttc gga ccc ggg gct ctg cgt		245
Val Gly Gln Leu Val Ala Thr Met Ser Phe Gly Pro Gly Ala Leu Arg		
60	65	70
gct agt ctg gtg cac gtg ggc agc cag cct cac aca gag ttt act ttt		293
Ala Ser Leu Val His Val Gly Ser Gln Pro His Thr Glu Phe Thr Phe		
75	80	85
gac cag tac agt tca ggc cag gct ata cgg gat gcc atc cgt gtt gca		341
Asp Gln Tyr Ser Ser Gly Gln Ala Ile Arg Asp Ala Ile Arg Val Ala		
90	95	100
ccc caa cgt atg ggt gat acc aac aca ggc ctg gca ctg gct tat gcc		389
Pro Gln Arg Met Gly Asp Thr Asn Thr Gly Leu Ala Leu Ala Tyr Ala		
105	110	115
aaa gaa caa ttg ttt gct gag gaa gca ggt gcc cgg cca ggg gtt ccc		437
Lys Glu Gln Leu Phe Ala Glu Ala Gly Ala Arg Pro Gly Val Pro		
125	130	135
aag gtg ctg gtg tgg gtg aca gat ggt ggc tcc agc gac ccc gtg ggc		485
Lys Val Leu Val Trp Val Thr Asp Gly Ser Ser Asp Pro Val Gly		
140	145	150
ccc cct atg cag gag ctc aag gac ctg ggt gtc acc atc ttc att gtc		533
Pro Pro Met Gln Glu Leu Lys Asp Leu Gly Val Thr Ile Phe Ile Val		
155	160	165
agc act ggc cga ggc aac ctg ttg gag ctg ttg gca gct gcc tcg gct		581
Ser Thr Gly Arg Gly Asn Leu Leu Glu Leu Leu Ala Ala Ala Ser Ala		
170	175	180
cct gcc gag aag cac cta cac ttt gtg gat gtg gat gat ctt cct atc		629
Pro Ala Glu Lys His Leu His Phe Val Asp Val Asp Asp Leu Pro Ile		
185	190	195
205	210	215
att gcc cgg gag ctg cgg ggc tcc ata act gat gcg atg cag cca caa		677
Ile Ala Arg Glu Leu Arg Gly Ser Ile Thr Asp Ala Met Gln Pro Gln		
220	225	230
cag ctt cat gcc tcg gag gtt ctg tcc agt ggc ttc cgc ctg tcc tgg		725
Gln Leu His Ala Ser Glu Val Leu Ser Ser Gly Phe Arg Leu Ser Trp		
235	240	245
ccg ccc ctg ctg aca gcg gac tct ggt tac tac gtg ctg gaa ttg gta		773
Pro Pro Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val		
250	255	260
cct agc ggc aaa ctg gca acc aca aga cgc caa cag ctg ccc ggg aat		821
Pro Ser Gly Lys Leu Ala Thr Thr Arg Arg Gln Gln Leu Pro Gly Asn		

gct acc agc tgg acc tgg aca gat ctc gac ccg gac aca gac tat gaa		869	
Ala Thr Ser Trp Thr Trp Thr Asp Leu Asp Pro Asp Thr Asp Tyr Glu			
265	270	275	280
gta tca ctg ctg cct gag tcc aac gtg cac ctc ctg agg ccg cag cac		917	
Val Ser Leu Leu Pro Glu Ser Asn Val His Leu Leu Arg Pro Gln His			
285	290	295	
gtg cga gta cgc aca ctg caa gag gag gcc ggg cca gaa cgc atc gtc		965	
Val Arg Val Arg Thr Leu Gln Glu Ala Gly Pro Glu Arg Ile Val			
300	305	310	
atc tcg cat gcg agg ccg cgc agc ctc cgc gta agc tgg gcc ccc gcg		1013	
Ile Ser His Ala Arg Pro Arg Ser Leu Arg Val Ser Trp Ala Pro Ala			
315	320	325	
ctt ggc ccg gac tcc gct ctc ggc tac cat gta cag ctc gga cct ctg		1061	
Leu Gly Pro Asp Ser Ala Leu Gly Tyr His Val Gln Leu Gly Pro Leu			
330	335	340	
cag ggc ggg tcc cta gag cgc gtg gag gtg cca gca ggc cag aac agc		1109	
Gln Gly Gly Ser Leu Glu Arg Val Glu Val Pro Ala Gly Gln Asn Ser			
345	350	355	360
act acc gtc cag ggc ctg acg ccc tgc acc act tac ctg gtg act gtg		1157	
Thr Thr Val Gln Gly Leu Thr Pro Cys Thr Thr Tyr Leu Val Thr Val			
365	370	375	
act gcc gcc ttc cgc tcc ggc cgc cag agg gcg ctg tcg gct aag gcc		1205	
Thr Ala Ala Phe Arg Ser Gly Arg Gln Arg Ala Leu Ser Ala Lys Ala			
380	385	390	
tgt acg gcc tct ggc gcg cgg acc cgt gct ccg cag tcc atg cgg ccg		1253	
Cys Thr Ala Ser Gly Ala Arg Thr Arg Ala Pro Gln Ser Met Arg Pro			
395	400	405	
gag gct gga ccg cgg gag ccc tgaactgcct gcctgctcgt ccacccgggg		1304	
Glu Ala Gly Pro Arg Glu Pro			
410	415		
gccctcttcc ctagccccga gagagagaca ctgctgctcg tgggtttct tgtggatgga		1364	
gtcgggtggg gagatggat gccggtcctg ccttgacca gcgttaattc cttcgtcgt		1424	
ttccccactg gtcatcgccg cccttgcctg acttccggga aacccggta gcctcacgcg		1484	
caatggcggt cctctccggt tgccagtgga gttgagcaca cggtggcct tgggcaactc		1544	
ttggcgaggg gatggacagt gtctgaggtc aggttggaga cataagaccc aggaaccgccc		1604	
ttcaggagag gaggccacag agttccaac ctgtgcacaa ggctggccc tctggatggca		1664	
gggactacgc atggcttga ggaggcggtc aggaccatcc aggtcctgcc tggcctaga		1724	
aagtggtag gagaagggaa agagagacta gtgttagacag gattcccgaa aacttcctca		1784	
aggaaaggaa agatagggag gtatgctggg aggctgtatga tggatggcattg gtttcatca		1844	

agatgtcctg ccagcctaga ggccgggatc tgtcagggtc actgactctg cttcctgcc 1904  
caggacctgc actggccct cgatcagtgc caaggatgca gtctttcac aggaatggga 1964  
cgagaccttg gcatttaggg cctcagggat aggagagccg cactatgaca gattctaagg 2024  
gagcctcctg cttagtgta gggagcaagg tgtcatgcag gtgggctacc tcctgccatc 2084  
accattaccc tggggcatct gacagatacc taagggtggt caggaacagg tttcctctca 2144  
agtccctatg taggcctctc ctctcctctc agaatcattt gccttatccc aagcttactc 2204  
catctcttcc ccactaatga cccggactct aacaacaata cagtcagaca gacataaact 2264  
tgccctgcag tctcattaaa atgctgtatt ttctgtcaaa aaaaaaa 2311